



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,147

DATE: 07/30/2003

TIME: 18:04:56

Input Set : A:\089147sq

Output Set: N:\CRF4\07302003\J089147.raw

3 <110> APPLICANT: Kindl, Helmut
 4 May, Christian
 5 Feussner, Ivo
 7 <120> TITLE OF INVENTION: The N-terminal beta-barrel structure of lipid body
 lipoxxygenase mediates
 8 its binding to liposomes and lipid bodies
 10 <130> FILE REFERENCE: 99_1235
 12 <140> CURRENT APPLICATION NUMBER: US 10/089,147
 C--> 13 <141> CURRENT FILING DATE: 2002-03-27
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP/00/09912
 16 <151> PRIOR FILING DATE: 2000-10-10
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: WordPerfect 6.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 732
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Cucumis sativus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(732)
 31 <400> SEQUENCE: 1
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 35 Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
 36 1 5 10 15
 38 gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat 96
 39 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
 40 20 25 30
 42 aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt 144
 43 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
 44 35 40 45
 46 atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt 192
 47 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
 48 50 55 60
 50 gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att 240
 51 Asp Asn Phe Thr Glu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
 52 65 70 75 80
 54 agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag 288
 55 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 56 85 90 95
 58 gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga 336
 59 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 60 100 105 110
 62 gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt 384
 63 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe

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64          115          120          125
66 cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc 432
67 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
68      130          135          140
70 aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt 480
71 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
72 145          150          155          160
74 gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc 528
75 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
76          165          170          175
78 att ttc ttt gcc aat cat gtt tat ctt cca agt caa aca cca aac cct 576
79 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
80          180          185          190
82 ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga 624
83 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
84          195          200          205
86 aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat 672
87 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
88      210          215          220
90 aat gac att gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt. 720
91 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
92 225          230          235          240
94 ggg acg acc gaa 732
95 Gly Thr Thr Glu
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 244
100 <212> TYPE: PRT
101 <213> ORGANISM: Cucumis sativus
103 <400> SEQUENCE: 2
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106 1 5 10 15
108 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
109 20 25 30
111 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
112 35 40 45
114 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
115 50 55 60
117 Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
118 65 70 75 80
120 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
121 85 90 95
123 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
124 100 105 110
126 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
127 115 120 125
129 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
130 130 135 140
132 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
133 145 150 155 160

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135 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
136                               165                               170                               175
138 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
139                               180                               185                               190
141 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
142                               195                               200                               205
144 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
145                               210                               215                               220
147 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
148 225                               230                               235                               240
150 Gly Thr Thr Glu
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 2964
154 <212> TYPE: DNA
155 <213> ORGANISM: Cucumis sativus
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (48)..(2684)
161 <400> SEQUENCE: 3
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164                               Met Phe Gly
165                               1
167 att ggg aag aac atc att gaa ggg gcc ttg aat aca act gga gat ctt 104
168 Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr Gly Asp Leu
169 5                               10                               15
171 gca ggt tct gtt atc aat gct ggt ggt aac att tta gat aga gtt tcc 152
172 Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp Arg Val Ser
173 20                               25                               30                               35
175 agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc 200
176 Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser
177 40                               45                               50
179 aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc 248
180 Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe
181 55                               60                               65
183 act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act 296
184 Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr
185 70                               75                               80
187 cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg 344
188 His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu
189 85                               90                               95
191 gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg 392
192 Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val
193 100                               105                               110                               115
195 ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt cca gga gct 440
196 Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe Pro Gly Ala
197 120                               125                               130
199 ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc aaa tct ctc 488
200 Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu
201 135                               140                               145

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203	act	ctt	gat	gat	gtt	cct	ggc	tat	ggc	aga	gtc	cat	ttt	gat	tgc	aat	536
204	Thr	Leu	Asp	Asp	Val	Pro	Gly	Tyr	Gly	Arg	Val	His	Phe	Asp	Cys	Asn	
205			150						155				160				
207	tct	tgg	gtt	tac	cct	tct	gga	aga	tac	aag	aaa	gat	cgc	att	ttc	ttt	584
208	Ser	Trp	Val	Tyr	Pro	Ser	Gly	Arg	Tyr	Lys	Lys	Asp	Arg	Ile	Phe	Phe	
209		165					170					175					
211	gcc	aat	cat	gtt	tat	ctt	cca	agt	caa	aca	cca	aac	cct	ctt	cgt	aag	632
212	Ala	Asn	His	Val	Tyr	Leu	Pro	Ser	Gln	Thr	Pro	Asn	Pro	Leu	Arg	Lys	
213	180					185					190					195	
215	tat	aga	gag	gaa	gaa	ttg	tgg	aat	ttg	aga	gga	gat	gga	aca	gga	gaa	680
216	Tyr	Arg	Glu	Glu	Glu	Leu	Trp	Asn	Leu	Arg	Gly	Asp	Gly	Thr	Gly	Glu	
217				200					205					210			
219	aga	aag	gaa	tgg	gat	aga	att	tat	gac	tat	gat	gtt	tat	aat	gac	att	728
220	Arg	Lys	Glu	Trp	Asp	Arg	Ile	Tyr	Asp	Tyr	Asp	Val	Tyr	Asn	Asp	Ile	
221			215						220				225				
223	gct	gac	cct	gat	gtt	ggt	gat	cat	cgt	cct	att	ctc	ggt	ggg	acg	acc	776
224	Ala	Asp	Pro	Asp	Val	Gly	Asp	His	Arg	Pro	Ile	Leu	Gly	Gly	Thr	Thr	
225			230				235					240					
227	gaa	tat	cct	tac	cct	cgt	agg	gga	aga	aca	gga	cga	cca	cga	tca	aga	824
228	Glu	Tyr	Pro	Tyr	Pro	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Pro	Arg	Ser	Arg	
229		245				250					255						
231	aga	gac	cac	aat	tat	gag	agc	aga	ttg	tca	cca	ata	atg	agc	tta	gac	872
232	Arg	Asp	His	Asn	Tyr	Glu	Ser	Arg	Leu	Ser	Pro	Ile	Met	Ser	Leu	Asp	
233	260				265				270					275			
235	atc	tat	gta	cca	aaa	gat	gaa	aac	ttt	ggg	cat	ttg	aag	atg	tca	gat	920
236	Ile	Tyr	Val	Pro	Lys	Asp	Glu	Asn	Phe	Gly	His	Leu	Lys	Met	Ser	Asp	
237				280					285					290			
239	ttc	ctt	ggt	tat	aca	tta	aaa	gca	ctt	tcg	ata	tca	atc	aaa	cca	gga	968
240	Phe	Leu	Gly	Tyr	Thr	Leu	Lys	Ala	Leu	Ser	Ile	Ser	Ile	Lys	Pro	Gly	
241			295					300					305				
243	ctt	caa	tcc	ata	ttt	gat	gta	act	cca	aat	gaa	ttt	gac	aat	ttt	aaa	1016
244	Leu	Gln	Ser	Ile	Phe	Asp	Val	Thr	Pro	Asn	Glu	Phe	Asp	Asn	Phe	Lys	
245			310				315					320					
247	gaa	gtt	gat	aat	ctc	ttt	gag	aga	ggt	ttt	ccc	att	cca	ttt	aat	gct	1064
248	Glu	Val	Asp	Asn	Leu	Phe	Glu	Arg	Gly	Phe	Pro	Ile	Pro	Phe	Asn	Ala	
249		325				330					335						
251	ttt	aag	acc	ctc	act	gag	gac	ctc	act	cca	cct	ttg	ttc	aaa	gca	ctc	1112
252	Phe	Lys	Thr	Leu	Thr	Glu	Asp	Leu	Thr	Pro	Pro	Leu	Phe	Lys	Ala	Leu	
253	340				345						350				355		
255	gtg	agg	aat	gat	ggt	gaa	aaa	ttc	ctc	aaa	ttt	cct	act	ccc	gaa	gtt	1160
256	Val	Arg	Asn	Asp	Gly	Glu	Lys	Phe	Leu	Lys	Phe	Pro	Thr	Pro	Glu	Val	
257			360						365					370			
259	gtc	aaa	gat	aat	aaa	ata	gga	tgg	agc	act	gat	gaa	gaa	ttt	gca	aga	1208
260	Val	Lys	Asp	Asn	Lys	Ile	Gly	Trp	Ser	Thr	Asp	Glu	Glu	Phe	Ala	Arg	
261			375						380					385			
263	gaa	atg	tta	gca	gga	ccc	aat	cct	cta	ttg	att	cgt	cgt	ctt	gaa	gct	1256
264	Glu	Met	Leu	Ala	Gly	Pro	Asn	Pro	Leu	Leu	Ile	Arg	Arg	Leu	Glu	Ala	
265			390				395					400					
267	ttt	cca	cca	aca	agt	aag	ctt	gac	cca	aat	gtt	tat	ggg	aat	caa	aac	1304

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268	Phe	Pro	Pro	Thr	Ser	Lys	Leu	Asp	Pro	Asn	Val	Tyr	Gly	Asn	Gln	Asn	
269		405					410					415					
271	agt	acc	atc	act	gaa	gaa	cac	ata	aag	cat	ggt	tta	gat	ggt	ctt	acg	1352
272	Ser	Thr	Ile	Thr	Glu	Glu	His	Ile	Lys	His	Gly	Leu	Asp	Gly	Leu	Thr	
273	420					425					430					435	
275	ggt	gat	gag	gca	atg	aag	caa	aac	agg	ctc	tac	ata	gtg	gat	ttc	cat	1400
276	Val	Asp	Glu	Ala	Met	Lys	Gln	Asn	Arg	Leu	Tyr	Ile	Val	Asp	Phe	His	
277					440					445						450	
279	gat	gca	tta	atg	ccc	tat	ctt	aca	agg	atg	aat	gca	aca	tca	aca	aaa	1448
280	Asp	Ala	Leu	Met	Pro	Tyr	Leu	Thr	Arg	Met	Asn	Ala	Thr	Ser	Thr	Lys	
281					455				460							465	
283	aca	tat	gcc	aca	aga	aca	ttg	ctt	ctt	ttg	aaa	gat	gat	ggg	act	ttg	1496
284	Thr	Tyr	Ala	Thr	Arg	Thr	Leu	Leu	Leu	Leu	Lys	Asp	Asp	Gly	Thr	Leu	
285			470				475						480				
287	aag	cca	ttg	ggt	att	gag	tta	gcc	ttg	cca	cat	cct	caa	gga	gat	caa	1544
288	Lys	Pro	Leu	Val	Ile	Glu	Leu	Ala	Leu	Pro	His	Pro	Gln	Gly	Asp	Gln	
289		485				490						495					
291	ctt	ggt	gcc	att	agc	aaa	cta	tac	ttt	cca	gct	gaa	aat	gga	ggt	caa	1592
292	Leu	Gly	Ala	Ile	Ser	Lys	Leu	Tyr	Phe	Pro	Ala	Glu	Asn	Gly	Val	Gln	
293	500					505					510					515	
295	aaa	tcc	att	tgg	caa	ttg	gct	aaa	gct	tat	gta	act	ggt	aat	gat	ggt	1640
296	Lys	Ser	Ile	Trp	Gln	Leu	Ala	Lys	Ala	Tyr	Val	Thr	Val	Asn	Asp	Val	
297					520					525						530	
299	ggc	tac	cat	caa	ctt	att	agt	cat	tgg	ttg	cat	act	cat	gct	gta	ctt	1688
300	Gly	Tyr	His	Gln	Leu	Ile	Ser	His	Trp	Leu	His	Thr	His	Ala	Val	Leu	
301					535				540							545	
303	gag	cca	ttt	gtg	att	gca	aca	cat	aga	caa	ttg	agc	gtg	ctt	cat	cca	1736
304	Glu	Pro	Phe	Val	Ile	Ala	Thr	His	Arg	Gln	Leu	Ser	Val	Leu	His	Pro	
305			550					555								560	
307	atc	cat	aag	ttg	ctt	ggt	cct	cat	tac	aaa	gac	act	atg	ttt	ata	aat	1784
308	Ile	His	Lys	Leu	Leu	Val	Pro	His	Tyr	Lys	Asp	Thr	Met	Phe	Ile	Asn	
309		565					570						575				
311	gca	tct	gca	aga	caa	ggt	ttg	atc	aat	gcc	aat	ggt	ctt	atc	gaa	aca	1832
312	Ala	Ser	Ala	Arg	Gln	Val	Leu	Ile	Asn	Ala	Asn	Gly	Leu	Ile	Glu	Thr	
313	580					585					590					595	
315	acc	cat	tat	cca	tca	aaa	tat	tca	atg	gag	ttg	tca	tct	atc	ttg	tac	1880
316	Thr	His	Tyr	Pro	Ser	Lys	Tyr	Ser	Met	Glu	Leu	Ser	Ser	Ile	Leu	Tyr	
317					600					605						610	
319	aag	gat	tgg	acc	ttc	cct	gat	caa	gca	tta	cct	aat	aat	ctc	atg	aag	1928
320	Lys	Asp	Trp	Thr	Phe	Pro	Asp	Gln	Ala	Leu	Pro	Asn	Asn	Leu	Met	Lys	
321					615					620						625	
323	aga	gga	cta	gct	gtg	gag	gac	tca	agt	gcc	ccc	cat	gga	ctt	aga	ttg	1976
324	Arg	Gly	Leu	Ala	Val	Glu	Asp	Ser	Ser	Ala	Pro	His	Gly	Leu	Arg	Leu	
325			630						635					640			
327	cta	ata	aat	gat	tat	cca	ttt	gct	ggt	gat	ggt	ctt	gac	att	tgg	tca	2024
328	Leu	Ile	Asn	Asp	Tyr	Pro	Phe	Ala	Val	Asp	Gly	Leu	Asp	Ile	Trp	Ser	
329		645					650						655				
331	gcc	att	aaa	aca	tgg	gta	cag	gat	tat	tgc	tgt	ctc	tac	tac	aaa	gat	2072
332	Ala	Ile	Lys	Thr	Trp	Val	Gln	Asp	Tyr	Cys	Cys	Leu	Tyr	Tyr	Lys	Asp	

VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date